Sequence 251, App Sequence 1988, Ap Sequence 81, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

sequence 38, 1 Sequence 522,

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence:

Run on:

Searched:

Database

Result No.

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Sequence 316, Application US/08961527

Sequence 316, Application US/08961527

Sequence No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRIE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.4%; Score 23.6; DB 4; Length 2453; 76.3%; Pred. No. 5.1; 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FEADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HE Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HE VECTE 486/33 COPERAING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/961,527
APPLICATION NUMBER: ASPAICANTON NUMBER: PRIOR APPLICATION NUMBER: BTOOKES, A. Anders REGISTRATION NUMBER: BS,373
REFERENCE/POCKET NUMBER: PB340P1
TELECOMMUNICATION NUMBER: PB340P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAACATTAAACAGCGTGCAATTACATATTGATAATCA 40
                                         US-09-134-001C-1459
US-09-134-001C-148-1
US-09-910-174B-1
US-08-961-527-251
US-08-961-527-251
US-08-942-008-1
US-08-942-008-1
US-09-164-138-27
US-09-634-238-27
US-09-634-286-3
US-10-254-869-3
US-10-254-869-3
US-10-254-869-3
US-09-276-531-63
US-09-322-938-38
US-09-322-938-38
US-09-322-938-38
US-09-322-938-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (301) 309-8504
TELEPAK: (301) 309-8512
INFORMATION FOR SEQ ID NO: 316:
SEQUENCE CHARACTERISTICS:
LENGTH: 2453 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 76.3
Matches 29; Conservative
                                               TYPE:
STRANDEDNESS: GOU
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US-08-961-527-316
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US-08-961-527-316
à
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                                                                                                                                                                                            March 22, 2004, 01:47:15; Search time 62 Seconds (without alignments) 402.787 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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(ogn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/RorTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/RorTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-961-527-316
US-09-328-352-3411
US-09-660-410-8
US-09-72-45-8
US-09-721-458-8
US-09-328-352-599
US-09-328-352-599
US-09-328-352-599
US-09-328-352-599
US-09-328-352-599
US-09-328-352-1397
US-09-328-352-1397
US-09-453-137-151
US-09-963-137-151
US-09-963-137-151
US-09-963-137-151
US-09-963-137-151
US-09-107-5328-1988
US-09-107-5328-1988
US-09-107-5328-1988
US-09-715-285-1
US-09-715-285-1
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US-09-596-002-7
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US-09-621-976-10105
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US-09-543-681A-1262
US-08-998-416-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             nucleic search, using sw model
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Maximum DB seq length: 200000000
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1647
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Gaps

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Sequence 8, Application US/09723458
Sequence 8, Application US/09723458
Patent No. 6586242
GENERAL INPORMATION:
APPLICANT: Cobb. Melanie
Chen, Zhu
Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 32;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGCAAACATTAAACAGGGTGCAATTACATATTGATAATCAGGTTC
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                                                 CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CONFINANCS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/060,410
FILING DATE: IH-APR-1998
CLASSIFICATION NUMBER: US/09/060,410
FILING DATE: IH-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAVIG J.
REGERENCE/DOCKET NUMBER: 860098.421
TELEFAMICA/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 360098.421
TELEFAMICA/DOCKET NUMBER: 360098.421
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,458
FILING DATE: 27-NO. 6586242-2000
CLASSIFICATION . cinknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: AUKKNOWN>
ATTORNEY, AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-060-410-8
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Sequence 1, Application US/08545528D
Sequence 1, Application US/08545528D
Setent No. 633773
GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION: Uncleotide Sequence of the Mycoplasma Genitalium Genome, Fragment Patent No. 653773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193P1
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
                                                                                                     GENERAL INC. 2015.00:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Sequence 8, Application US/09060410

Patent No. 6165461

GENERAL INFORMATION:

APPLICANT: Cobb, Melanie

APPLICANT: Chon, Zhu

APPLICANT: Berman, Kevin

TITLE OF INVENTION: THEREFOR

NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21.6; DB 4; Length 723;
Pred. No. 24;
0; Mismatches 14; Indels
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Best Local Similarity 69.0%; Pred. No. 89;
Matches 29; Conservative 0; Mismatches
                                   US-09-328-352-3411/c
; Sequence 3411, Application US/09328352
; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), ORGANISM: Acinetobacter baumannii
US-09-328-352-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.2%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580073
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                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 341:
LENGIH: 723
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
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Gaps

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Sequence 1397, Application US/09328352
Patent No. 6662958
Patent No. 666296
GENERAL INFORMATION:
APPLICAMY: Gary L. Breton et al.
APPLICAMY: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
GURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1397
LENGTH: 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
FILE REFERENCE: GTC99-03PA
CURRENT FAPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1032 AGCCAAAGTATAATCGCGTGTAATTGCAGATGGATTATCCGACTC 988
                                                                                                                                                                                                                                                                                                                           369 adcharchcrachdddigdachachcringidhddachighrific 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 786;
                                                                                                                                                                                                       Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCAAACATTAAACAGCGTGCAATTACATATTGATAATCAGGTTC 45
                                                                                                                                                                                                                                                                                    1 AGCAAACATTAAACAGCGTGCAATTACATATTGATAATCAGGTTC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 ACTAAAACAGGATCAAGTACATATTGATAGTCAGGAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ATTANACAGCGTGCAATTACATATTGATAATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.7%; Score 21; DB 4; Best Local Similarity 73.0%; Pred. No. 40; Matches 27; Conservative 0; Mismatches 10
                                                                                                                                                                                                     Score 21; DB 4;
Pred. No. 39;
0; Mismatches 1
                                                                      ORGANISM: PORYPHYROMONAS GINGIVALIS FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-328-352-599/C
Sequence 599, Application US/09328352
; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Acinetobacter baumannii
  DNA (genomic)
                                                                                                                                                                                                   46.7%;
Local Similarity 66.7%;
nes 30; Conservative
                                                                                                                    NAME/KEY: misc feature;
; LOCATION: 1...614
US-09-221-017B-1040
MOLECULE TYPE: DNA (HYPOTHETICAL: NO ANTI-SENSE: UNKNOWN ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-328-352-1397/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-328-352-1397
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                                                                                                                                                                                                         Query Match
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Matches
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Pred. No. 32;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                       1 AGCAAACATTAAACAGCGTGCAATTACATATTGATAATCAGGTTC 45
                                                                                                                                                                                                                                                                                                                                                                                                            AGAAAAACTITAAAGGCCCATGGAAATGCAAATTAAAAAAACAGTTTC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,392
REFERENCE/FOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP1546
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 10-DEC-1998
PRIOR APPLICATION NUMBER: PC7AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:

NUMBER: PC7AU98/10123
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MONITOY, Gladys H
REGISTRATION NUMBER: 32,430
REFRENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPAX: 650-813-560
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1040:
SEQUENCE CHARACTERISTICS:
                                                                              TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       LENGTH: 190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 614 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                   US-09-723-458-8
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Gaps

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TYPE: DNA
ORGANISM: Mus musculus
US-09-963-137-151
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US-09-963-137-151/c
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ZIP: 53701-213

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible
OCHEVER: IBM PC compatible
OCHEVER: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION NDATE: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION NOWBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CRASSIFICATION NUMBER: 06/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay. Nicholas J.
REFERENCE/DOCKET NUMBER: 3386
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 2643;
                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 4; Length 264
Pred. No. 48;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGCAPACATTAAACAGCGTGCAATTACATATTGATAA 37
US-09-486-072-6/c
| Sequence 6, Application US/09486072
| Sequence 6, Application US/09486072
| Patent No. 6489155
| CHERRAL INFORMATION:
| APPLICANT: Masanori TRKAYAMA, et al.
| TITLE OF INVENTION: GENES
| FILE REPERENCE: 11202/1
| CURRENT APPLICATION NUMBER: US/09/486,072
| CURRENT FILING DATE: 2000-02-22
| PRIOR FILING DATE: 1997-09-03
| NUMBER OF SEQ ID NOS: 30
| SOOTHARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 6
| LENGTH: 2643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 73.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                       TYPE: DNA
; ORGANISM: Bacteria
US-09-486-072-6
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US-09-963-137-151/c

Sequence 151, Application US/09963137

Patent No. 6596036

GENERAL INFORMATION:
APPLICANT: Pedersen, Finn S

APPLICANT: Pedersen, Finn S

APPLICANT: Nelsen, Annette B

APPLICANT: Moving, Helle
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR LYMPHOWA AND LEUKEMIA

APPLICANT: Moving, Helle
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR LYMPHOWA AND LEUKEMIA

PRICE REPERENCE: A-70981/RMS/DCF
CURRENT APPLICATION NUMBER: US 09/965,137

CURRENT FILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-09-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-09-24

PRIOR PRIOR FILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-09-24
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Sequence 178, Application US/09963137

Sequence 178, Application US/09963137

Sequence 178, Application US/09963137

Setent No. 6556036

GREEN INFORMATION:

APPLICANT: Sorensen, Annette B

APPLICANT: Hernandez, Javier Martin

APPLICANT: Nielsen, Anne A

APPLICANT: Moving, Helle

TITLE REPERENCE: A 70981/RMS/DCF

FILE REPERENCE: A 70981/RMS/DCF

CURRENT APPLICATION NUMBER: US/09/963,137
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                                                                                                                                                                                                                                        Query Match

46.7%; Score 21; DB 4; Length 46819;
Best Local Similarity 73.0%; Pred. No. 75;
Matches 27; Conservative 0; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42743 ACAATAAACTGCCGCCAATCAGATACAGAGACTCAGG 42707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                                                                                                                            6 ACATTAAACAGCGTGCAATTACATATTGATAATCAGG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20.8; DB 4;
Pred. No. 60;
0; Mismatches 12;
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 72:

US-09-453-702B-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0%;
Matches 28; Conservative
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KB: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or
NAME/KB: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or
NAME/KB: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
                       NAME/KEY: misc feature
LOCATION: (559241). (559241)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (600992). (600992)
OTHER INPORVATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (622708). (622708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (312837)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (312993)
OTHER INFORMATION: n equals a, t
        OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gequence 1, Application US/08916421B

Patent No. 6503729

GENERAL INFORMATION:

APPLICATION Complete Genome Sequence of the Methanogenic Archaeon, Methanococ

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: PB275

CURRENT FILING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: US 60/024,428

PRIOR FILING DATE: 1996-08-22

PRIOR FILING DATE: 1996-08-22

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3:1

SEQ ID NO 1

LENGTH: 1664976

TYPE: DNA

CREANTS: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.8; DB 4; Length 3. Pred. No. 60; 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1574 Accarrcagcarccracaagaacararrarrarrarrarrar 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AACATTAAACAGCGTGCAATTACATATTGATAATCAGGTT 44
CURRENT FILING DATE: 2001-09-24

PRICR APPLICATION NUMBER: US 09/668,644

PRICR FILING DATE: 2000-09-22

PRICR FILING DATE: 2001-07-13

PRICR FILING DATE: 2001-07-13

PRICR FILING DATE: 2001-07-13

PRICR FILING DATE: 2001-07-13

PRICR APPLICATION NUMBER: US 09/962,929

PRICR FILING DATE: 2001-09-24

PRICR PILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 215

SEQ ID NO 178

LENGTH: 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY MANY KEY: misc feature
LOCATION: (28222)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (84812)...(84812)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
COCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Mus musculus
US-09-963-137-178
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influenzae Rd Genome, Fragments
                                                                                                                                                                  APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influencae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1830121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784657 AACGTHATATCGCGTGCCAATACACTTTGTAAATCAACTT 784696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Nucleotide sequence of
the Haemophilus influenzae
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AACATTAAACAGGGTGCAATTACATATTGATAATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 28; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:

MEDINA TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIPICATION: «URNOWN»

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNAY AGENT INTORNATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REPERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPAX: 301-309-8439
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-557-884-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09643990A
patent No. 6528289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucle
RESULT 14
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-643-990A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1077378 AAAATTAAATTACATACAGTCAAAGATTGATGATGTTT 1077339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1349473)
LOCATION: (1349473)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1349491)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1470091). (1470091)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1569020). (1569020)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1602912). (160212)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1603744). (1603734)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1603794). (1603734)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1603798). (1603734)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (16037980). (1637998)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                        LOCATION: (779455). (779455)
LOCATION: (779455). (779455)
OTHER INFORMATION: n equals a, t, NAME/KEX: misc_feature of the coration: (779676). (779676). (779676). (779676). (779676). (779676). (779676). (779676). (7796770). (855539). (855539). (855539). (855539). (9716710N: n equals a, t, NAME/KEX: misc_feature of the coration: (871619). (7716710N: (871619). (1871619). (7796710N: (184830). (1084830). (1084830). (10968410N: n equals a, t, NAME/KEX: misc_feature of the coration: (19684830). (19684830). (19684810N: n equals a, t, NAME/KEX: misc_feature of the coration: (19684810N: n equals a, t, NAME/KEX: misc_feature of the coration: (19684810N: (19684810N: n equals a, t, NAME/KEY: misc_feature of the coration: (19684810N: n equals a, t, NAME/KEY: misc_feature of the coration: (19684810N: n misc_feature of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (111981). (111981).
OTHER INFORMATION: nequals a, t.
NAME/KEY: misc_feature
LOCATION: (113681). (113081).
OTHER INFORMATION: nequals a, t.
NAME/KEY: misc_feature
LOCATION: (1310989). (1310988).
OTHER INFORMATION: nequals a, t.
NAME/KEY: misc_feature
LOCATION: (1313224). (1313224). (1313224).
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc_feature
                                                                                                       LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
       LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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Gaps

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Wed Mar 24 10:55:58 2004
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us-10-018-878-9.rni

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STATE: MD

COUNTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

COMPUTER: Dell CATION

SOFTWARE: ASCII TEXT

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 13-40g-2000

CLASSITCATION NUMBER: 08/426,787

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-06-07

ATTORNEY/ASTI INFORMATION:

REGISTRATION NUMBER: 40,302

REGISTRATION NUMBER: 40,302

REGISTRATION NUMBER: 40,302

REFERENCE/COCKET NUMBER: 40,302

TELEFONE: 301-610-5790

TELEFONE: 301-610-5790

TELEFONE: 301-610-5790

TELEFONE: 301-610-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

46.2%; SCOPE 20.8; I

OND NO: 1:

OND NO: 1:
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784657 AACGTTATATCGCGTGCCAATACACTTTGTAAATCAACTT 784696

Gaps

Query Match 46.2%; Score 20.8; DB 4; Length 1830121; Best Local Similarity 70.0%; Pred. No. 1.2e+02; Matches 28; Conservative 0; Mismatches 12; Indels 0; C

S AACATTAAACAGCGTGCAATTACATATTGATAATCAGGTT 44

Search completed: March 22, 2004, 04:12:34 Job time : 89 secs

us-10-018-878-9.rnpb

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Sequence 9, Appli
Sequence 127515,
Sequence 55144, A
Sequence 142, App
Sequence 1215, App
Sequence 3804, Ap
Sequence 12215, A
Sequence 129, App
Sequence 6062, Appli
Sequence 612976,
Sequence 238109,
Sequence 238110,
Sequence 238110,
                                                                                                                                  March 22, 2004, 03:57:11; Search time 1651 Seconds (without alignments) 100.825 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCTUB_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/DS08_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                             1 agcaaacattaaacagcgtg......acatattgataatcaggttc
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-345-492-9
2 US-10-424-599-127515
2 US-10-424-599-55144
5 US-10-085-117-142
2 US-10-158-844-316
2 US-09-938-842A-3804
1 US-09-938-842A-3804
1 US-09-910-943-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-020-141-5
US-10-032-585-6062
US-10-424-599-123076
US-10-027-632-238110
US-10-027-632-238110
                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            2438257 segs, 1849576744 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                          US-10-018-878-9
45
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Perfect score:
                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
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Sequence 955, App Sequence 1811, Appli Sequence 1. Appli Sequence 1. Appli Sequence 752, App Sequence 752, App Sequence 752, App Sequence 25552, Sequence 16854, Sequence 15599, Ap Sequence 15653, Sequence 16863, Sequence 15653, Sequence 15653, Sequence 156362, Sequence 156363, Sequence 156364, App Sequence 1674, App Sequence 17, Appl Sequence 17, Appl Sequence 23, Appli Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 27, Appli Sequence 27, Appli Sequence 8, Appli Sequence 
   US-10-094-749-955
US-10-027-633-2202630
US-10-311-455-1851
US-10-11-455-1851
US-10-067-514-1
5 US-10-067-514-1
5 US-10-067-514-1
1 US-10-067-632-16895
US-10-027-632-16895
US-10-027-632-16895
US-10-027-632-16996
US-10-027-632-16996
US-10-027-632-16996
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US-10-037-632-16966
US-10-037-632-16966
US-10-037-632-16966
US-10-037-632-16966
US-10-038-133-1455-1071
US-10-282-124-444
US-10-384-388-23
US-10-282-1744-44
US-10-311-455-494
US-10-282-1744-44
US-10-282-1744-44
US-10-282-1744-44
```

ALIGNMENTS

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Gaps
Sequence 9, Application US/09345492

Sequence 9, Application US/09345492

Patent No. US2020128457A1

GENERAL INFORMATION

APPLICANT: LIU, LIN

APPLICANT: LOU, LIN

APPLICANT: WANG, BAOMIN

TITLE OF INVENTION: VERGEY

TITLE OF INVENTION: PEOXYRIBONUCLEOSIDES PRODUCTION

FILE REFERENCE: 28460/123

CURRENT APPLICATION NUMBER: US/09/345,492

CURRENT APPLICATION NUMBER: US/09/345,492

CURRENT FILING DATE: 1999-07-01

SOFTWARE: PATENT NOS: 9

SOFTWARE: PATENT NOS: 9

SOFTWARE: PATENT NOS: 9

SOFTWARE: PATENT NOS: 9

SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:

† OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-345-492-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGCAAACATTAAACAGCGTGCAATTACATATTGATAATCAGGTTC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-10-424-599-127515/c
i Sequence 127515, Application US/10424599
; Publication No. US20640031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
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APPLICANT: Kunsch et al.
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 193357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186434 ATCAACCCTTCATAAGCGTGCCATCACATTGGATCAACAGGT 186392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGCAAACATTAAACAGCGTGCAATTACATATTGATAATCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.4%; Score 23.6; DB 12; Best Local Similarity 76.3%; Pred. No. 1.7e+02; Matches 29; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
52.9%; Score 23.8; DB 15;
Best Local Similarity 72.1%; Pred. No. 4.5e+02;
Matches 31; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CAAACATTAAACAGCGTGCAATTACATATTGATAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: DD-I Latitude Pentium 3
COMPUTER: DB-I Latitude Pentium 3
COPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Unn-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340PlD1
INFORMATION FOR SEQ ID NO: 316:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTONNEX/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 316:
                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 142
LENGTH: 193357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12215, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-158-844-316; Sequence 316, Application US/10158844; Publication No. US20040029118A1; GENERAL INPORMATION:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-12215/c
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Sequence Signature of the control of
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Publication No. US20030232334A1
Publication No. US20030232334A1
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REPERENCE: 529452000117
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.3%; Score 24; DB 12; Length 421; Best Local Similarity 75.0%; Pred. No. 77; Matches 30; Conservative 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 agccaactaraaaaaccrtrcaargaraaatrgaraarca 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGCAAACATTAAACAGCGTGCAATTACATATTGATAATCA 40
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Pred. No. 1.1e+02;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_20806C.1
US-10-424-599-55144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: PAT_MRT3847_86150C.1
US-10-424-599-127515
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Best Local Similarity 72.1%;
Matches 31; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max FEATURE:
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APPLICANT: La Rosa Thomas J

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Sequence 129, Application US/09910943

Patent No. US20020081610A1

GENERAL INFORMATION:

APPLICANT: Hemmati-Brivanlou, Ali

APPLICANT: Hemmati-Brivanlou, Ali

APPLICANT: Hemmati-Brivanlou, Ali

APPLICANT: Hemmati-Brivanlou, Ali

PILLE PERERENET: 759/16148051

CURRENT APPLICATION UNDER: US/09/910,943

CURRENT APPLICATION UNDER: US/09/910,943

SOFTWARE: Patentin version 3.1

SEQ ID NO:29

LENGHIH: 71

PERMONET: 201

SEQ ID NO:29

SEQ ID NO:29

SEQ ID NO:29
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51.1%; Score 23; DB 9; Length 771;
Best Local Similarity 74.4%; Pred. No. 2e+02;
Matches 29; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 CAAGTATTAATCATCGTACGATTACATGTTCATATTAAGTT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CAAACATTAAACAGCGTGCAATTACATATTGATAATCAGGT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.0%; Score 23.4; DB 11; Best Local Similarity 73.2%; Pred. No. 1.9e+02; Matches 30; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) LOCATION: (1) 7(771)

; OTHER INFORMATION: n may be a or g or c or t/u

US-09-910-943-129
                                                                                                                                  FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,942A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3804
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Arabidopsis thaliana
US-09-938-842A-3804
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ORGANISM: Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1)..(771)
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US-09-910-943-129
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Patent No. US20020160378A1

Patent No. US20020160378A1

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: APPLICANT: Wang, Xun

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC FLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REPRENCE: SCRIP3300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PRING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111
...valic David K

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 12215

TYPE

TYPE
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US-09-938-642A-3804/c

US-09-938-642A-3804/c

Sequence 3804, Application US/09938842A

Publication No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: Kreps, Joff

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STARSS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.4; DB 12; Length Pred. No. 1.4e+02; 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_111038C.1
US-10-424-599-12215
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.2%;
Matches 30; Conservative
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SEQ ID NO 3804
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Glycine max
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US-09-938-842A-3804/c
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US-10-027-632-238110
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; ORGANISM: Human
US-10-027-632-238109
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Sequence 123076, Application US/2046031072A1
Sequence 123076, Application NO. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Con Yonwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 123076
LENGTH: 288
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Sequence 6062, Application US/10032585
Sequence 6062, Application US/10032585
Sequence 6062, Application Wo. US20030180953A1
Sequence 6062, Application Wo. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Bo. Jiang
APPLICANT: Charles Boone
APPLICANT: Howard, Bussey
TILE REFERENCE: 1018-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 6062
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                                                                                                                                                                       Length 183337;
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                                                                                                                                                                    Query Match 51.1%; Score 23; DB 14; Length 18
Best Local Similarity 74.4%; Pred. No. 8.4e+02;
Matches 29; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                             132374 GCCAACATTTTACTGTCTGCAAATAGATATTCCTAATCA 132336
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OTHER INFORMATION: unsure at all n locations
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Candida albicans
                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Glycine max
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Sequence 238110, Application US/10027632

Publication No. US2003020407549

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/02/03/06

PRIOR FILING DATE: 2000-07-12

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PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: US 60/167,363
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/27,632

CURRENT APPLICATION NUMBER: US/2010.06

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Query Match

49.8%; Score 22.4; DB 12; Length 288;
Best Local Similarity 70.7%; Pred. No. 2.6e+02;
Matches 29; Conservative 0; Mismatches 12; Indels 0.
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49.8%; Score 22.4; DB 15;
Best Local Similarity 72.5%; Pred. No. 3.2e+02;
Matches 29; Conservative 0; Mismatches 11;
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's Sequence 228109, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:
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| PRIOR FILING DATE: 1999-09-09
| SOFTWARE: Exersor for Windows Version 4.0
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| Watches 29; Conservative 0; Vision 4.0
| Watches 29; Conservative 0; Windows Version 4.0
| SALCATTACON WINDER: US 60/193, 483
| PRIOR FILING DATE: 2000-03-29
| CURRENT FAILED FOR PRILICATION WUNDER: US 60/186, 218
| PRIOR FILING DATE: 2000-03-29
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| PRIOR PRILING DATE: 1
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